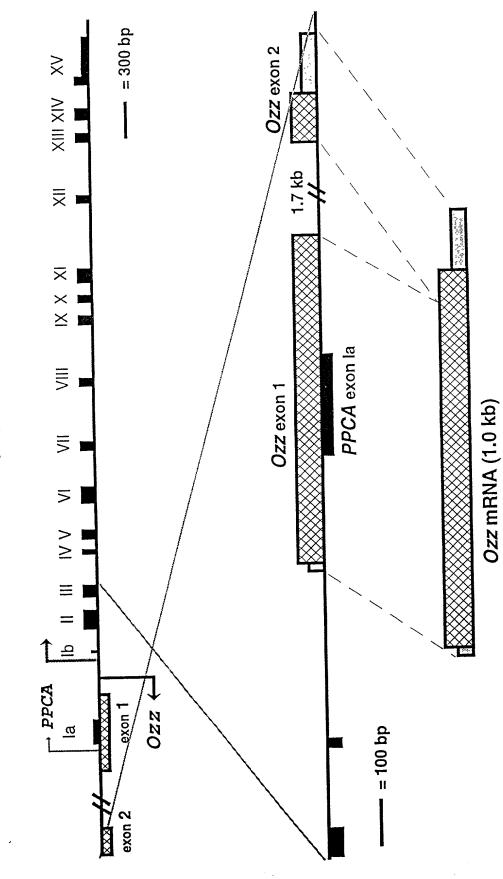
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FIG. 2A

1	CCCTGTTGCA	CGGCTTGGAG	ATG GCTGCTC	CCTCCGAACA	CGTAGGACTG
51	GGTGCCCCAC	GGAGCCCTGC	GCGCCCAGAG	CCCCCTCCCA	CCCGCTTCCA
101	CCAAGTGCAT	GGAGCCAACA	TCCGCATGGA	CCCCTCAGGA	ACGCGAGCCA
151	CACGCGTGGA	GAGTTTCGCC	CACGGTGTGT	GCTTCAGTCG	TGAGCCCCTG
201	GCCCCGGCC	AGGTATTTCT	AGTGGAAATT	GAGGAAAAAG	AGCTGGGCTG
251	GTGCGGGCAC	CTACGTCTTG	GCCTGACCGC	TCTGGATCCC	GCCAGTCTGG
301	CCGCTGTACC	CGAGTTTTCA	CTGCCTGACT	TGGTCAGCCT	TGGCCACAGT
351	TGGGTCTTCG	CTATCACACG	CCACCACAAC	CGTGTGCCCC	GGGAAGGTCA
401	ACCAGAAGCG	GAGGCAGCGG	TCCCCAGTGG	TCCCCAAGCC	CTACTGGTTG
451	AACCCTATCT	GCGCATCGAG	CAGTTCCGAA	TTCCCCGGGA	CCGTCTGGTG
501	GGCCGCAGCC	GGCCAGGGCT	TTATAGCCAC	CTCTTAGATC	AGCTCTATGA
551	ACAAAACGTG	CTGCCTCCTA	CAGCGCGCCG	AAGCCGCTTG	GGTGTTCTCT
601	TCTGCCCCCG	TGAGGATGGG	ACCGCCGACA	TGCACATCAT	CATCAACGGG
651	GAGGACATGG	GCCCTAGCGC	CCGGGGGCTG	CCAGCTGCTC	AGCCCCTCTA
701	CGCTGTGGTA	GATGTGTTTG	CTTCCACCAA	GAGCGTGCGT	CTGGTCCAGC
751	TGGAGTATGG	CTTGCCATCT	CTGCAGACTC	TGTGCCGACT	AGTGATCCAG
801	AAGAGGGTGG	TACACAGGCT	GGCCATTGAT	GTGCTCCACC	TGCCCAAAGG
851	ACTGAAGGAC	TTCTGCAAGT	ACGAA TGA AC	GAATGAACGC	CTGTCTGTGG
901	CCACCAGAGC	AAAGTCCCCG	GTGGTGCGCC	CTGCCTCTAG	AGAAGTGGCT
951	AGTCTGAAGC	TGGTCGCACA	GCTCACAATC	AGGGCTGGAA	ATAAATAGAG
1001	CCGATGTGGA	TGTTCTGAGA	ААААААААА	AAAAA	

FIG. 2B

GCCCAAAGAA CTTAAGGATT TCTGCAAGTA TGAGTGAAGA CCCACAGTGC ACCAGAGCAC AGCTGCATCC GCGGTGGTGG ACGTGTTTGC TTCCACAAAG AGCGTGCGCC TTGTCCAGCT CGAGTATGGC TTGCCATCCC TGCAGACTCT GTGCCGCCTA GTGATACAAA GGAGCATGGT GCACCGGCTG GCCATTGATG GGCTCCACCT GCACATCATC ATCAACGGCG AGGACATGGG CCCGAGCGCC CGGGGGACTGC CAGCTGCGCA GCCCCTCTAC TGCCTCCGAC CGCGCCGT AGCCGCCTGG GTGTCCTCTT TTGCCCGCGC CCCGATGGCA CGGCCGACAT CGCCTGGTGG GCCGCAGCCCG GCCAGGGCTC TACAGCCATC TCTTGGACCA GCTCTATGAG CTGAACGTGC GGGTCTTCGC CATCACGCGC CACCACAACC GCGTGCCCCC GGAGGGCCGC CCGGAGGCGG AGGCAGCGGC CCCCAGCCGA CCTCCAACCC TCCTCGTGGA ACCATATCTG CGCATTGAGC AGTTTCGCAT TCCCCGGGAC GGICTICCIG GICGAGAICG AGGAGAAAGA GCIGGGCIGG IGCGGACAIC IGCGICTCGG ICTGACCGCG CIGGACCCCG CCAGICIGGC CCCCGIICCC GAGITITICIC IGCCCGAICI GGICAACCIG GGCCACACCI CGCGGGCCAC ACGCGTGGAG AGCTTCGCCC ACGGCGTGTG CTTCAGCCGC GAGCCGCTGG CCCCGGGCCA CCTGCCCTAT GGCCGAGAGA TGGCTGCTGC CTCCGAGCCC GTGGATTCGG GTGCACTCTG GGGACTCGAG CGCCCGGAGC CCCCTCCCAC CCGCTTCCAT CGGGTGCACG GTGCCAACAT CCGCGTGGAC CCCTCTGGGA TEGAGCCCCA GACCTGTGGC TGGCTGGTCC GAAGTTGGCC ACATTGCTGC CAGCCAAGAC

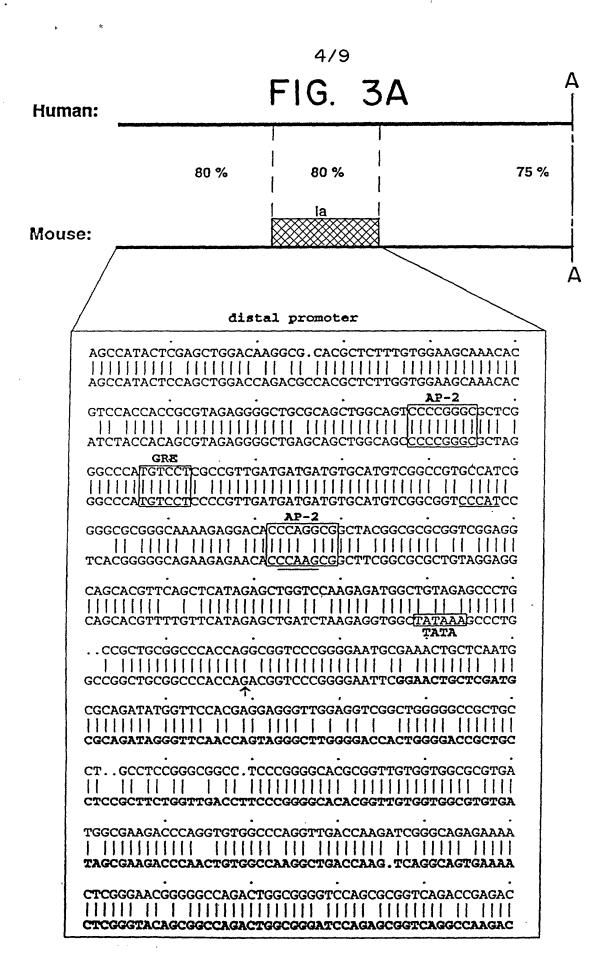
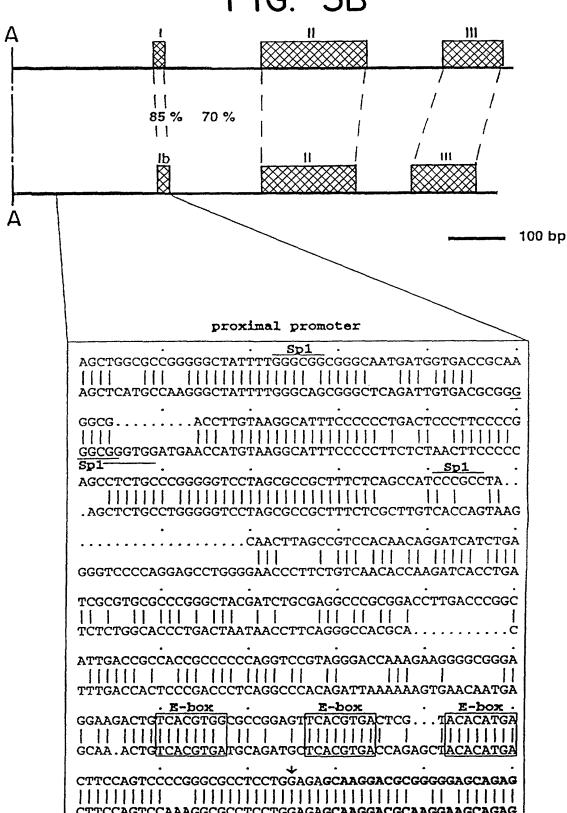


FIG. 3B



-box (P/hxS/T/PLQH/YhCRxxhxxxhx2-10hxxLPhPxxhxY/FLx1-3Y/F)	Tyrosine kinase-phosphorylation site	BC-box (T/SL/MxxxC/SxxxV/L/I)
SOCS - box (P/hxS/T/PLQH/	Casein kinase II −phosphorylation	Protein kinase C-phosphorylation site

9 9 MAAASEPVDSGALWGLERPEPPPTRFHRVHGANIRVDPSGTRATRVESFAHGVCFSREPL MAAPSEHVGLGAPRSPARPEPPPTRFHQVHGANIRMDPSGTRATRVESFAHGVCFSREPL RPEPPPTRFH+VHGANIR+DPSGTRAKKVESFAHGVCFSREPL GA MAA SE V ч mouse: human:

120 120 APGQVFLVEIEEKELGWCGHLRLGLTALDPASLAAVPEFSLPDLVSLGHSWVFAITRHHN **APGQVFLVEIEEKELGWCGHLRLGLTALDPASLAPVPEFSLPDLVNLGHTWVFAITRHHN** APGQVFLVEIEEKELGWCGHLRLGLKALDPASLA VPEFSLPDLV+LGH+WVFAITRHHN 61 human:

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180 RVPREGRPEAEAAAPSRPPTLLVEPYLRIEQFRIPRDRLVGRSRPGLYSHLLDQLYELNV 121 61 mouse:

human:

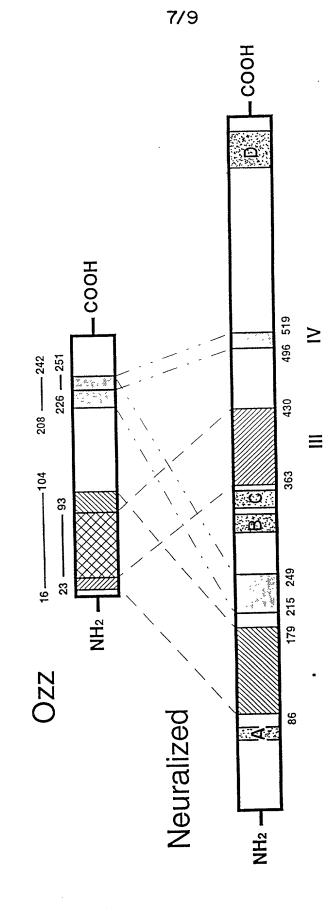
180 RVPREGQPEAEAAVPSGPQALLVEPYLRIEQFRIPRDRLVGRSRPGLYSHLLDQLYEQNV RVPREG+PEAEAA PS P LLVEPYLRIEQFRIPRDRLVGRSRPGLYSHLLDQLYE NV 121 240 LPPTARRSRLGVLFCPRPDGTADMHIIIINGEDMGPSARGLPAAQPLYAVVDVFASTKSVR LPP<u>NARR</u>SRLGVLFCPR DGTADMHIIINGEDMGPSARGLPAAQPLYAVVDVFASTKSVR 181 human:

LPPTARRSRLGVLFCPREDGTADMHIIINGEDMGPSARGLPAAQPLYAVVDVFASTKSVR 181 mouse:

285 LVQLEYGLESKOTKORKVIORSWYHRKAIDGCHKREKKBFCKKE LVQLEYGLPSLQTLCRLV1Q+ +VHRLAID LHLPK LKDFCKYE 241 human:

LVQLEYGLPSKRTKSACXTOKRYVARKATOVLHCRKOCKBECKYE 241 mouse:

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FIG. 6

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S Z > > _ _ _ O C Ozz Neu A O W 4 क क क I < ပ > ≯≻ ს∑ 70 MIN œ> - μ メト വ ന 四天 S a I വ ഗ <u>a – </u> **4** & A R E Ozz Neu Ozz Neu \equiv

OZZ A L D R A S L Neu S C M R L L L

NT. RH メ**ナ** のの CT S Q O တ္တ **4** & **4** ⊢ 40 n N LÞ ഗ **–**

FIG. 7

